

WHAT IS CLAIMED IS:

Dkt C1

1. A mutant  $\alpha$ -amylase obtained by making replacement or deletion of at least one residue of amino acid residues 5 respectively corresponding to the 11th Tyr, 16th Glu, 49th Asn, 84th Glu, 144th Ser, 167th Gln, 169th Tyr, 178th Ala, 188th Glu, 190th Asn, 205th His and 209th Gln in the amino acid sequence set forth in SEQ ID NO:1 in an  $\alpha$ -amylase having said amino acid sequence, or an  $\alpha$ -amylase having a 10 homology of at least 70% to said amino acid sequence.
2. A mutant  $\alpha$ -amylase obtained by making replacement of a sequence corresponding to 11 to 100 amino acid residues from the amino terminal in the amino acid sequence set forth in SEQ ID NO:1 in an  $\alpha$ -amylase having 15 said amino acid sequence, or an  $\alpha$ -amylase having a homology of at least 70% to said amino acid sequence by an amino acid sequence of another liquefying  $\alpha$ -amylase corresponding to said sequence of the amino acid residues.
- 20 3. The mutant  $\alpha$ -amylase according to Claim 2, wherein a sequence corresponding to amino acid residues from the 1st Asp to the 19th Gly in the amino acid sequence of SEQ ID NO:1 is replaced by an amino acid sequence of another liquefying  $\alpha$ -amylase corresponding to 25 said amino acid sequence.

*Sub C1*

4. The mutant  $\alpha$ -amylase according to Claim 2 or 3, wherein said another liquefying  $\alpha$ -amylase has the amino acid sequence set forth in SEQ ID NO:2.

*Sub A*

5 5. A mutant  $\alpha$ -amylase obtained by introducing a mutation into an  $\alpha$ -amylase having the amino acid sequence set forth in SEQ ID NO:1 or an  $\alpha$ -amylase having a homology of at least 70% to said amino acid sequence with at least two kinds of replacement or deletion selected from the

10 10. replacement or deletion of the amino acid residues set forth in Claim 1, and the replacement of the amino acid sequence set forth in any one of Claims 2 to 4 combined with each other.

*Sub C1*

15 6. The mutant  $\alpha$ -amylase according to Claim 5, wherein the replacement of the amino acid residue comprises replacing an amino acid residue corresponding to the 11th Tyr in the amino acid sequence of SEQ ID NO:1 by Phe, an amino acid residue corresponding to the 16th Glu

20 20. by Pro, an amino acid residue corresponding to the 49th Asn by Ser, an amino acid residue corresponding to the 167th Gln by Glu, an amino acid residue corresponding to the 169th Tyr by Lys, an amino acid residue corresponding to the 190th Asn by Phe, an amino acid residue

25 25. corresponding to the 205th His by Arg, or an amino acid residue corresponding to the 209th Gln by Val, and the replacement of the amino acid sequence comprises replacing

an amino acid sequence from the 1st Asp to the 19th Gly in the amino acid sequence of SEQ ID NO:1 by an amino acid sequence from the 1st His to the 21st Gly in the amino acid sequence set forth in SEQ ID NO:2.

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7. A gene encoding the mutant  $\alpha$ -amylase according to ~~any one of claims 1 to 6~~, or a vector containing said gene.



8. Cells transformed by the vector according to

10 Claim 7.

Claim 1  
Claim 2  
Claim 3  
Claim 4  
Claim 5  
Claim 6

9. A process for producing a mutant  $\alpha$ -amylase, comprising culturing the transformed cells according to Claim 8.

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10. A detergent composition comprising the mutant  $\alpha$ -amylase according to ~~any one of claims 1 to 6~~.



add D  $\Rightarrow$  add E  $\Rightarrow$